

Figure 2: Nucleotide sequence of TbP15
Sheet 2 of 4

TTCTCGGCTTTTGCTGGCTTTGCTCACATGTTCTTCTCGCTGCTTATCCCTTGATTCTGTGGAT
AACCCTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCGCGAGCCGAACAGCCAGCGCAGCGAG
TCAGTGAGCGAGGAAGCGGAAGAGCGCCTGATGCGGTATTTCTCCTTACGCATCTGTGCGGTATT
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CACTCCCGTATCGCTACGTGACTGGGTCTATGGCTGGCGCCCGACACCCGCAACACCCGCTGACGCG
GCCCTGACGGGCTTGCTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTG
CATGTGTACAGAGGTTTTCACCGCTCATCACGAAACCGCGAGGCGAGCTGCGGTAAAGCTCATCAGC
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TGATGCCCTCCGTGTAAGGGGATTTCTGTTTCATGGGGTAATGATACCGATGAACAGAGAGGAT
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GACGAAGGCTTGAGCGAGGCGGTGCAAGATTTCGAATACCGCAAGCGACAGCGCGCATCTGCTGCC
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ATTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTCCGGAACCTGTGCTGCCAGCTGCATTAATG
AATCGGCCAACCGCGCGGGAGAGGCGGTTTGCTATTGGCGCGCAGGGTGGTTTTTCTTTTCAACA
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CGCTGGTTTGCCCGCAGCGCGAATACTCTTTGATGGTGGTTAACCGCGGGATATAACATGAGC
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TGGCGCGCATTTGCGCCAGCGCATCTGATCGTTGGCAACAGCATCGCAGTGGGAACGATGCCCT
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TCGGCTGAAATTTGATTGCGAGTGAGATATTTATGCCAGCCAGCCAGACGCGACCGCGGAGACAG
AACTTAATGGGCGCGTAAACAGCGCGATTTCGCTGGTGAACCAATGCGACAGATGCTCCACGCGCA
GTGCGGTACCGTCTTCATGGGAGAAAAATAACTGTTGATGGGTGATGCTGCGGATTTAATCGAGAA
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CGCTTCGTTTACCATTCGACACACCGGCTGGCAACCCAGTTGATGCGCGGAGATTTAATCGCGG
CGACAATTTGCGACGGCGCGTGCAGGGCCAGACTGGAGGTGGCAACGCCAATCAGCAACGAGTTT
TGCCCGCGAGTTGTTGTGCCACCGGCTTGGGAATGTAACTCAGCTCCGCGCATCGCGCTTCCACTT
TTTCCCGCGTTTTTCGCAAAAGCGTGGCTGGCTGGCTGGTTCAACCGCGGGAACGGTCTGATAAGAGA
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ACCATACCCACGCGAACAAGCGCTCATGAGCCGGAAGTGGCGAGCCGATCTTCCCATCGGTG
ATGTCGGCGATATAGCGCCAGCAACCGCACTGTGGCGCGGTTGATGCGCGCCAGATGCTGCCG

Figure 2: Nucleotide sequence of TbF15
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GCGTAGAGGATCGAGATCTCGATCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGG
 ATRAACAATTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAGGAGATATACATATGGGCCATCA
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 GCTGTTCAACCTGTGGGGTCCGGCTTTTACGAGAGGTATCCGAACGTCAAGATCACCGCTCAGGG
 CACCGGTTCTGGTGC CGGGATCCGCGAGGCGCGCGCGCGGACGGTCAACATTTGGGGCTTCGACGC
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 TCAGCAGGTCAACTACAACTGCCCCGAGTGAGCGAGCACCTCAAGCTGAACGGAAGTCCCTGGC
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 GAACCTGCCCGGCACCGCGGTAGTTCCGCTGCACCGCTCCGACGGGTCCGGTGACACCTTCTTGTT
 CACCCAGTACCTGTCCAGCAAGATCCCGAGGGCTGGGGCAAGTCCGCCGCTTCGGCACCCGCT
 CGACTTCCCGCGGTGCCCGGTCCGCTGGGTGAGAACCGCAACCGCGCATGGTGACCGGTTGCGC
 CGAGACACCGCGCTCGGTGGCTTATATCGGCATCAGCTTCTCGACAGGCGCAGTCAACGGGACT
 CGCGAGGCCCAACTAGGCAATAGCTCTGGCAATTTCTTGTTGCCCGACCGCAAGCATTCAGGC
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 CGACGAGGAGCAGCAGCAGGCGCTGTCTCGCAATGGGCTTTACTCAGTCCGACACCGTGACCGT
 GGATCAGCAAGAGATTTTGAACAGGGCCAACGAGGTGGAGGCCCGATGGCGGACCCACCGACTGA
 TGTTCCCATCACACCGTGCGAACTCACCGCGCTTAAACCGCGCCCAACAGCTGGTATTTGTCCGC
 CGCAACATCCGGGAATACCTGGCGCGCGGTGCCAAAGAGCGGCAGCGTCTGGCGACCTCGCTGGC
 CAACCGCGCCAAAGCGTATGGCGAGTTGATGAGGAGGCTCGGACCGGCTGGACAAACGAGCGCGA
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 AGTCCGGCTCGAACCGGCTTTACGCGGAACCCCTTCCGCCCGCGACCAATTTCTCCCGGTGACGC
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 CGCACGATGGTTCCGCTACCGCTACCGGATCGCGCGGTGGTGGCTTCCCGCTGACACGGCGCGCAGCT
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Figure 2: Nucleotide sequence of TbF15
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GCGGCCCGCTGGCGCTGGTGACATTGCCGGCTTAGGCCAGGGAAGGGCCGGCGGCGGCGCGCGCT
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CGCTCGAGCACCACCACCACCACCTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGT
TGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGG
GTTTTTGTGAAAGGAGGAACCTATATCCGGAT

Figure 3: Amino Acid Sequence of TbF14

MQHHHHHTDRVSVGNLRIARVLYDFVNNEALPGTDIDPDSFWAGVDEKVVADLTPONQALLNARDE
 LQAQIDKWHRRRVIEPIDMDAYRQFLTEIGYLLPEPDDFTITTSQGVDAEITTTAGPQLVVPVLNAR
 FALNAANARWGSGLYDALYGTQDVI PETDGAEGKGPYTNKVRGDKVIAYARKFLDQSVPLSSGSGFGDAT
 GFTVQDGGQLVVALPKSTGLANPGQFAGYTGAARESPYSVLLINHGHLIEILIDPESQVGTDDRAGV
 KDVILESAITTIMDPEDSVAADVDAADKVLGYRNWLGKGLAAAVDKDGTAFRLVLRNDRNYTAP
 GGGQPTLPQRSIMFVRNVGHLMINDAIVDTDQSEVPEGIMDALPTGLIAIHGLKASDVNGPLINSR
 TGSIVIVKPKMHGPAEVAFTCELFSSRVEDVLGLPQNTMKIGIMDEERTTNNLKACIKAAADRVVF
 INTGFLDRTGDEIHTSMRAGPMVRKGTMTKSQPWILAYEDHNVDAGLAAGFSGGAQVKGKGMWTMTTEL
 MADMVETKIAQPRAGASTAWVFSPTAATLHALNYHQVDVAARVQQLAGKRRATISQLLTIPLAKEL
 AWAPDEIREEVNNQCSILGYVVRNVQGGVCCSKVPDIHDVALMEDRATLRISSQLLANWLRHGV
 TSADVRASLERMAPLVDRQNAQDVAYEPMAPNFDDSI AFLAAQELILSGAQQPNGYTEPI LHRRRR
 EFKARAAEKPA PSDRAGDDAARVQKYGGSSVADAERIRRVAAERIVATKKQGNDDVVVVVSAMGDDTDD
 DLLDLAQQVC PAPPPEELDM LTAGERISNALVAMATIESLGAHARSFTGSQAGVITTGTHGNAKII
 DVTFGRLQTALEBGRVVLVAGPQGVSGDQTKDVTTLGRGGSDTTAVAMAAALGADVCEIYTDVDGIF
 SADPRIVRNARKLDTVTFEEMLEMAACGAKVLMRLRCVYARRHNI PVHVRSSYSRPGTIVVVGSIK
 DVPMEDPILTGVAHDRSEAKVTI VGLPDI PGYAAKVFRVARRRRQHRHGAAERLQGRGRQDRHHL
 HLLPQTSQPPFWKNWTRSETRSASTQLLYDDHIGKVS LIGAGMRSHPGVTATFCEALAAVGVNIEL
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Figure 4: Amino Acid Sequence of TbF15

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 TAQGTGSCAGIAQAAAGTVNIGASDAYLSEGDMAAHKGLMNIALAISAQVNVNLPQVSEHLKING
 KVLAAMYQGTIKTWDDPQIAALNPQVNLPGTAVVPLHRSDBGSGDTFLFTQYLSKQDPEGWGKSPGF
 GTTVDFPAVPGALGENGGMVTGCAETPGCVAYIGISFLDQASQRGLGEAQLGNSSGNFLLPDAQ
 SIQAAAGPASKTTPANQAI SMIDGPAPDGYPI INYEYAI VNNRQKDAATAQTLQAFLHWAITDGNK
 ASFLDQVHFQPLPPAVVVLSDALIATISSAEMKTDAAATLAQEAGNFERISQDLKTQIDQVESTAGS
 LQQQWREGAAGTAAQAAVVRPQEAANKQKQELDEISTNIRQAGVQYSRADEEQQALSSQMGTQSQ
 TVTVDDQSEILNRANEVEAPMADPPTDVPITPCELTAAKNAAQQLVLSADNMREYLAAGAKERORLA
 TSLRNAAKAYGEVDEEAATALDNDGEGTVQAESAGAVGGDSSASLTDTPHVATAGEPNFMDLKEAA
 RKLETGDCQASLAHFADGWNITPNLTLQGDVKKRFRGFDNWEQDAATACEASLDQQRQWILHMAKLSA
 AMAKQAQYVAQLHYWARREHPTTYEDIVGLERLYAENPFSARDQILPVYAEVQORSEKVLTEYNNKAA
 LKPVNPPKPPPAIKIDPPPPRQEQLIPGLMPSPDGSQVTPGTGMFAAPMVPPTGSPGGGLPADT
 AAQLTSAGREAAALSGDVAVKAASLGGGGGGVPSAPLGSALGGAESVVRPAGAGDIAGLGQGRAGG
 GAALGGGGMCMFMGAHQGGGAKSKGSQDEALYTTEDRAWTEAVIGNRRRQDSKESK.

Figure 5

	Status	TbF15	TbF6
5004	TB	0.926	1.043
7004	TB	0.928	0.184
9004	TB	1.102	1.135
11004	TB	0.856	1.819
15004	TB	2.035	2.059
17004	TB	2.493	2.286
18004	TB	0.471	10.412
21004	TB	0.061	1.615
23004	TB	0.425	0.591
26004	TB	0.296	0.392
27004	TB	0.244	0.207
28004	TB	2.236	2.04
30004	TB	0.052	1.508
32004	TB	2.374	1.927
33004	TB	1.508	1.378
34004	TB	0.059	1.136
36004	TB	0.546	1.105
37004	TB	1.446	1.989
39004	TB	0.021	2.782
41004	TB	0.311	0.652
43004	TB	0.355	0.433
44004	TB	0.131	0.66
53004	TB	0.109	0.317
FD8-24	Control	0.183	0.314
FD8-25	Control	0.061	0.063
FD8-26	Control	0.066	0.142
FD8-27	Control	0.021	0.115
FD8-28	Control	0.053	0.289
FD8-29	Control	0.114	0.248
FD8-30	Control	0.105	0.146
FD8-31	Control	0.101	0.237
FD8-33	Control	0.080	0.071
FD8-34	Control	0.140	0.117
FD8-35	Control	0.088	0.072
FD8-36	Control	0.081	0.089
FD8-37	Control	0.057	0.06
FD8-38	Control	0.104	0.111
FD8-39	Control	0.221	0.241
FD8-40	Control	0.257	0.265
FD8-41	Control	0.056	0.093
FD8-42	Control	0.184	0.273
FD8-43	Control	0.126	0.126
FD8-44	Control	0.193	0.092
FD8-45	Control	0.058	0.057
FD8-46	Control	0.183	0.23
FD8-48	Control	0.062	0.085
FD8-49	Control	0.134	0.247
Mean		0.113	0.157
SD		0.061	0.086
Mean +3SD		0.298	0.414
Sensitivity		22/23	20/23

HKL-1 (1-125)

Page 1

Monday, July 29, 1996 10:48 AM

FOC(1-129) Map.MPO (1 x 411) 8 nt. Quenes

enzymes: All 315 enzymes (No Hwv)

primers: Circular, GenBank Sites Only, Standard Genetic Code

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~~TACGTAGCTGGTAGTCTGGTAGTGTACTCGCTCGCAAGTAGTAGTATGGTTGCTAGTCAAGGTATCTCCGAACTATGCTGGAAGACCTGTAAGT~~

~~M R N H N H N H N H S R A T T I O P T L S A K O G L Y C L L G I G~~
~~AAATACCCACCAAGGGGTATCGCTTTACTCTCTCACTAGACTACTTCGAAAPAGCCCTGGAGGACCTGGCAGCAGCGCTTCCCGGTGATGGCT~~ 132

~~TTATGGCTTGGTTCCCGCATAGGAAATGAGGATGATCTGATGAAGGCTTTTCGGGACCTTCGTAAGCCCTGTGCAAGACCGCGACTACCG~~ 136
~~I P N Q G G L Y S S L E Y F E X A L E S L A A A P P G G G~~

~~GGTTAAGCTTCGGCCCGCGAGCAAAAGCCCGCAAAACCGCAACAGCTGAATTTTTCGAGGAGCTGGCAGACCTTCGATCTGCACTCATC~~ 278
~~CCAAATCCAGCCCGCGGCTGTGTATCGGCGCTTTTTCGGCTTGGTGCACCTTAAAGAGCTCTTGAACCTCTCGGAGCTAGCAGCTCGAGTAG~~

~~W E Q S A K O K Y A Q N R N H V N F F G E L A O L D R B L A~~
~~AGGCTGATCCAGGACAGGCGCAAGCCGGTCCAGACGACCGCGAGCTCTGAGGCCCGCCAGAGAGGCTTCAAGTTTCGCGGCGCGCTGGC~~ 368

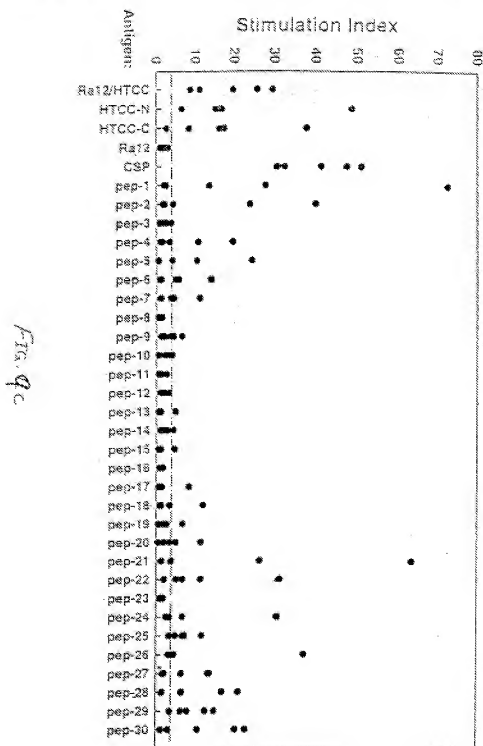
~~TGGACTAGGTCTGTGTCTGGTTCTCCCGAGGCTCTGTGGGCTGTAGAGCTTCCCGGTTCTTTTCAGAGCTCAAGACACCGGCTACCG~~ 368
~~S L I N G G A N A Y D T T R D I L E S R K K G L E F V R P A A~~

~~TGTGGAGCTGACCTACATCCCGCTGTGGGACGCTTATAG~~ 411
~~ACAGCTGGAGCTGGATGTAGGCGCAGAGCCCGCTCGCGGATATC~~

~~V O L T Y I P V V G N A L~~

Fig. 7c

T Cell Epitope Mapping of HTCC-1



Friday, July 23, 1993 8:47 AM
 57001361-5102 Mac.MPQ (1 x 1225) 38.1 Sequence

[illegible]

Monday, July 28, 1998 2:42 PM

[illegible]

2. *Staphylococcus aureus*

Figure 2

CGTGGCGGAGCTGATGATTTCTGATACCGGAGCGAAGCTCTTTGGGGGAAAAGACCCCGCGCGATCGCGGCTTAAAGAGGCGGATATACGGGCGAGATGCT

7243

60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 0

68AGCCGAGACCGCCTGGCAATGTTTGGGTACCTTCCTGGAACGGCGACTGCACAGGGCAACGTTGCTGCTGTAAGAAGCAAGCCGCGCGAAT

CCCCGGATTCTGCGGCGGGCGCTACAAAGCGATGCGCGCGCGGTCGTCGTCGCGCGCTGCGCGCTGCAAGGACCGGAAAGCTGCGCGCGCGCGCTGTA

• **Factor**

Q U A R T E R L Y J O U R N A L O F T H E A M E R I C A N S O C I E T Y O F P O L I T I C A L S C I E N C E S

5'GCGAGGCGCGGTCGGCTCC TCGAGGAGGCGCGCTGTCGAGGAGGCGCTCCGATCCCGCTCGCGGCGAGCCAGTGGATGAGAGTGTGCTCC

CTGGTGGGCGCCGACGCGAGGAGCTGGTCCGAGGAGCGGCTAGCTGCTCCGAGAGGGTGTGGGCGGCGCGCGCTGGGTCAAGTACCTGCTGTTACACGCGG

—T—E

T E A Q G L L E O A A A V S S A S Q I A A A N O L N N V P

UAGGCGCTGCAATAGCTGAGCCGAGTCCAGCGAGGGTACCAAGCCCTGCTTCCAGGCAGGCTGCTGCTCCCTGTCGAGAGAGACGGTCCTGCGCGCATCTGGT

GTCCGCGACGTTGTTGACCGGCTCGGTTCCGTTCCCTGTGTCGGAAGAACGTTCCGACCCACCGGACACCTTCTGCGCAGCGCGCTAGCGCA

— 72 —

Q A L G G L A C P I G C T P S S X L C C L W K T Y S P N R

CCCCGATCAGCAACATGGTGTCTCAATGGTCAACCAACCATGTGCGATGACCAAGTCCGGTCTGTCTCGATGACCAACACCTTGAGCTCGATGTTT

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TIME

U S N A V Y S H I P R E C O R D

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1000

X C F A P A L A A D A F C : A A C W D Y A A A A S S L C S S L

58TFTTCSGGTCFAGGCCGFGGGSTGGGCGGCAACTTGGGTGGGCGGGCCFCGGTGGGTTCGTTCGCGGTCGCGGAGGCC*GGGCTGGGG

LCAGAAAGCCAGACCCGCGAC (T)CACCGCCGCTTGAACTCAGGCTGXCCTGAGTCAGGCTCAAGCAAGAGCCACCGCCCTCCGATGCGCCGCG

— TEXAS

G S G L G G Y A A B L G H A A C V O Q + 20 Y P O X W X X

CGAAGCAGGGAATACCCGGGGGGCTGGGTGCCTACCAGGCTTAACTAGGGGGGGCAAGAGAGGCCCTGGGACAGATGCCTGGGCTG

[illegible]

— 104 —

A N O A Y T P A A R A L E L P Z L T S A L A R A P G G H L A V

9-CTGCGAGTGACCCASA TGGGGGCCAGCACCAGTGGTGGGTGAGTGAATGGCTGGTGTTCGGCGGCACCCATAATTAATCGCAATCT

CGACGGGCAAGCCCGTCTACCCGCGGTCCCAGGCCAACCAGCAGATCTCTAAACAAGAGCAAGAAGGCGGTC

104

L P Y O E H G A H A G G L S W Y L R Y P P X P Y S H P X S

Fig. 11

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Figure 1: Nucleotida sequence of MTb59

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 cccggtcggccagccgagtcgacgcggcgccggagagcgtcgactccgataccggcgccgctggaggt
 ccaggcgccctcggcggtgacccggcgaaggcgtgaaggagccggttcgacagaccgggatcaaggcgtat
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 gttgct

14

Figure 1: Amino acid sequence of MTb59

MAELTIIPADDIQSAISEYVSSFTADTSRSEVGTVVVDAGDGIHVEGLPSVMTQZELLEFPQGGILGVA
 LNLDEHSVGAVILGDFENISEGQVVKRTGEVLSVPVGDGFLGRVWNPLGQPIDGRGDVDSOTRRAL
 ELQAPS VWHRQGVKEPLQTGIKAIDAMTPIGRGQROLIIGDRKTGKTAVCVDTILNQRQNWESGDP
 KKQVRCVYVAIQQKGTITAAVR2TLEEGGANDYTTIVAAAASESAGFFONLAPYTGSALAHNMYESG
 KGVLIIPDDLTKQAGAYRAISLLLRFPGR2AYPGDVFFYLHGRLL2PCAKLSODLGGGSLTGLPII
 ETKANDISAYIPTNVISITDQCFL2DPLFNQGV2PAINVGVSVSRVGGAAQIKAMKEVAGSLRLD
 LSQYRELEAFAAFASDLDAASKAQLERGARLV2ELLKQP2SQPMPVEEQVVSIFLGTG2GHLD2VPVE
 DVRRFPETELLDHMRASEE2ILTEIRDSQKLTE2AADKLTEVIKNFK2G7AATGGGSVVPDEHVEAL
 DEDKLAKEAVKVKKPAK2KKK

16

Figure : Amino acid sequence of MTb82

MAKASETERSGPGTQPADAAQTATSATVRPLSTQAVFRPDPFGDEDNFPHPTLGPDTETPQDMATTISR
 VRPPVRRLLGGGLVEIPRAPDIDPLEALMTNPFVVPESKRFCWNCORPVGRSDSETKGASEGWCPPYCG
 SPYSFLPQLNPGDIVAGQYEVKGCIAHGGLWIXLALDRNVNGRPVVLKGLVHSGDAEAQAMAMAE
 RQFLAEVVRHPSIVQIFNFVEHTDERGDPVGYIVMEYVGGQSLKRSKQKLPVAZAIAYLLEILPAL
 SYLHSLGLVYNDLKPENIMLTETZQLKLIDLCVSRINSFGYLYGTPGFQAPEIVRTGPTVAIDIVT
 VORTLAALTLDLPTRNGRYVVOGLPEDDPVLKTYDSYGRLLRRAIDPDPRQRFTTASENSAQLTCVL
 REVVAQDTGVPRPGLSTIFSPSRSTFGVDLLVAHTDVYLDGQVHAEKLTANEIVTALSVPFLVDPDT
 VAASVLQATVLSQPVTLSGLRAARHGALDADGVDFSESVELPLMEVRALLDLQDVAKATRKLDL
 AERVGVWRRLVWYRAVAELLTGDDYSATKHFTFVLDTPFGDLAPKLALAAAGLAGNTDENKFFVQT
 VNSTNDGVISAAGFLARARSAEGDRVCAVRTLDEVPPTSRHFTTARLTSAVTLLSGRSTSEVTEZQ
 IRDAARRVEALPPTPEPRVLQIRALVLGGALDWLKDKNKASTNHILGFPFTSHGLRLGVEASLRSLAR
 VAPTQRHRYTLVDMANKVRPTSTF.

17

Figure 17: Amino Acid Sequence of secreted Dppp

DPPDPHQPDMTKGYC9GGRWGFGLAVCDGEEKYPDGSFWHQNMQTWFTG2QFYFDCVSGGE2LP
G29PPGCGCGAIFSEQPNAP

SEQUENCE LISTING

Mtb41 (MTCC#3)

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAGGTTGCTG	GCAATGAGT	TGGGGTTTT	ACCTCCGAA	GTGATTCAA	GGCGAATGA	60
TTCCGGTCCG	GGGCGGAGT	CGATGCTAGC	CGCGCGGGCC	GGCTGGGAGC	GTGTGGCCGC	120
GGAGTTGACT	TCCGCGCGCG	TCTGGTATCG	ATGGGTGGTG	TGGACGCTGA	TCGTTGAGCC	180
GTGGATGGGG	CGCGCGCGCG	CGCGGATGCG	GGGCGCGGCA	ACGCGGTATG	TGGGTGGGCT	240
GGCGCGGACG	GGCGCGCTGG	CGAAGGAGAC	GGCCACACAG	GGGAGGGGAG	CGGCGGAAGC	300
GTTTGGGAGC	CGGTTGCGCA	TGACGGTGCC	ACCATGCTTC	GTGGCGGCGA	ACGCGAGCGG	360
GTTGATGTGG	CTGGTGGCGG	CGAACATTC	GGGCGAAAC	AGTGGCGCGA	TGGGGGCTAC	420
CGAGCGGAG	TATGCGGAAA	TGTGGGCGCA	AGACGCTGCC	GTAATGTACA	GCTATGAGGG	480
GGCATCTGGG	GGCGGCTGGG	CGTTGCGCGC	GTTCACCTCA	CGGCTGCAAG	GCACGGGCGC	540
GGCGCGGCGC	GGCGCGCGAC	CGCGCGGCGC	CGAAGCGCGC	GGTGGCGGGG	CGGTTGCGGA	600
TGCACAGCGG	AGACTGCGGC	AGCTGCGCGC	GGGATCCCTG	AGCGACATTC	TGTGCGGATT	660
GGCGCGCAAC	GCTGATCGCG	TGACATCGGG	ACTGTTGGGG	ATCGGCTGCA	CGCTCAACCC	720
GCAAGTCGGA	TCCGCTCAGC	CGATAGTGGT	CGCCACCCCG	ATAGGGGAAT	TGGAGCTGAT	780
CGCGCTCTAC	ATTGATCCGA	TGGCGACCGG	CAGCATTCGG	CTCGGATGCA	CGAACACGGC	840
CAGACCTCGG	CACATCGCGC	TATACGGGAA	CGCGCGCGGG	CTGGGAGCGA	CGGAGGGGCA	900
TCCACTGAGT	TGGCGGACCG	ACGAGCGCGA	CGCGCACTGG	GGCGGCTTCG	GGGCGCGGCG	960
CGCGGCTGTC	CGCGGCGTGG	CGACGCGCGC	ATTAGTGGGA	GGGTTGTCGG	TGCGCGACAG	1020
CTGGACCGAG	CGCGCGCGCG	AGATCCAGCT	CGCGGTTGAG	GCACACCGCA	CGTTGACGTC	1080
CAGCGCGCGG	GGCGAGCGGA	CGGCGCTAAA	CGGAGTGCGG	GCAGGCTTCG	TCAGCGGGAT	1140
GGCTTTGGCG	AGCGCTGGCG	CAGCGCGCAC	GACGGCGCGT	GGCGGCACCC	GTAGCGGCGC	1200
CAGCACTGAC	GGCGAAGAGG	ACGCGCGCAA	ACCGCGGGTA	GTGTGATTA	GAGAGCGAGC	1260
CGCGCGCGGA	AACCGCGCGC	GGTAAAGTTC	CGGCGACCGT	TGCTCGCGCG	GGGAAAAATG	1320
CTCGGTGAGC	GTGGCTATCC	GACGGCGCGT	TCACACCGCT	TGTAGTAGCG	TACGCGCTATG	1380
GACGACGGTG	TCTGGATTCT	CGGCGGCTAT	CAGAGCGGAT	TGCTCGGCAA	CCTCAGCAAA	1440
G						1441

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Met	Asp	Phe	Gly	Leu	Leu	Pro	Pro	Glu	Val	Asn	Ser	Ser	Arg	Met	Tyr
1				5				10					15		
Ser	Gly	Pro	Gly	Pro	Glu	Ser	Met	Leu	Ala	Ala	Ala	Ala	Ala	Trp	Asp

20 25 30
 Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
 18 40 45
 Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
 50 55 60
 Met Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
 65 70 75 80
 Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
 85 90 95
 Phe Gly Thr Ala Phe Ala Met Thr Val Pro Ser Leu Val Ala Ala
 100 105 110
 Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
 115 120 125
 Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
 130 135 140
 Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
 145 150 155 160
 Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
 165 170 175
 Ala Gly Pro Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
 180 185 190
 Ala Val Ala Asp Ala Glu Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
 195 200 205
 Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
 210 215 220
 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
 225 230 235 240
 Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
 245 250 255
 Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
 260 265 270
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
 275 280 285
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
 290 295 300
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
 305 310 315 320
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
 325 330 335
 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
 340 345 350
 Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
 355 360 365
 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
 370 375 380
 Gly Thr Thr Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
 385 390 395 400
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Ile Arg Glu Gln Pro
 405 410 415
 Pro Pro Gly Asn Pro Pro Arg
 420

Mtb40 (HTCC#1)

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```

CAGCGATGAG CAGAGCGGTC ATCATCGATC CAACGATCAG TGCCATTGAC GGCTTGATCG      60
ACCTTCTGGG GATTGGAATA CCCAACCAAG GGGGTATCCT TTAAGCTCTA CTAGAGTACT      120
TCGAAAAAGC CCTGGAGGAG CTGGCAGGAG CGTTTCGGGG TGATGGCTGG TTAGGTTCCG      180
CCGCGGACAA ATACGCGCGC AAAAAGCGCA ACCACGTGAA TTTTTCCTAG GAAGTGGGAC      240
ACCTCGATCG TCGGCTCATC AGCCTGATCC ACCAGCAGGC CAACCCGGTC CAGACGACCC      300
GGGACATCCT GAGAGGCGCC AAGAAAGGTC TCGAGTTCCT GCGCCCGGTG GCTGTGGAGC      360
TGACCTAGAT CCGCGTCTCT GGGCAGCGCC TATCGGCGGC CTTCGAGGCG CGGTTTGGCG      420
CGGGCGGGAT GGGCGTAGTG GCGGGCGGCG TTGCGTACTT GGTGCTGAAA ACGCTGATCA      480
ACGCGACTCA ACTCCTCAAA TTGCTTGCCA AATTGCGGGA GTTGCTGGCG GCGGCCATTG      540
CGGACATCAT TTGGATGTGT GCGGACATCA TCAAGGGCAC CCTCGAGAAA GTGTGGAGT      600
TCATCACAAA CCGCTCAAC GGGCTGAAG AGCTTTGGGA CAAGCTCACG GGGTGGGTGA      660
CGGAGTGTCT CTCTCGAGGG TGGTGAAGC TGGAGTCTCT CTTTGGCGGC GTCCCGGCT      720
TGACCGGCGC GACGAGCGGC TTGTGGCAAG TGACTGCTT GTTGGGTGGG GCGGCTCTCT      780
CGGATGCTCT GGGCTTGCTT CACGCGGATA CCGTGGGAG CTCACGAGC TTGCGCGGCT      840
TGGCGGCGAT TGGGGGAGGG TCGGCTTTTG GGGGCTTGGC GAGGCTGGCT CAGGTCGATG      900
CGGCTCAAC TGGGCAAGCG CTACGCGCCC GAGCTGATGG CCGGCTGGCG GCGGCTGGCG      960
AGCAGGTGGG CGGCGAGTGG CAGCTGGTTC CCGGCGAGGG TTCCCAAGGT ATGGCGGAGC      1020
CGGTAGGCAT GCGCGGCGAT CACGCTCTTT CGGGGCGCTC GAAAGGACG ACGACGAGAA      1080
AGTACTCGGA AGCGCGCGCG GCGGCGACTG AAGACGCGGA GCGCGCGGCA GTCGAGCTGG      1140
ACGGGGGCGG TGGGCAAAAG GTGCTGTATC GAAAGCTGCT CTAAGCGCAT GCGGAGCCAA      1200

```

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Xle Ser Ala Ile Asp Gly
  1           5           10
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
          20          25          30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
        35          40          45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
        50          55          60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
        65          70          75          80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
        85          90          95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
       100       105       110

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Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
 115 128 125
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
 130 135 140
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
 145 150 155 160
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
 165 170 175
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
 180 185 190
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
 195 200 205
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
 210 215 220
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
 225 230 235 240
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 245 250 255
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
 260 265 270
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
 275 280 285
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
 290 295 300
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
 305 310 315 320
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
 325 330 335
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
 340 345 350
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
 355 360 365
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
 370 375 380
 Lys Val Leu Val Arg Asn Val Val
 385 390

Mtb9.9A (MTI-A)

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xii) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGCTCTCTT TCAAGTCAT AAGTTCGGT GGCAGTCGG CCGCGCGTGC ATAAGGCACC
 AATAACGCGT GTCCATGGA TACCCGACC GCACGACGGT AGACGGGATC AGCCGACCG

60
 120

GTGCGGAACA	CTACCGGCTC	CACGCTCAGC	CCTGCCGCGT	TCCGGAAGAT	CGAGCCGAGG	180
TTCTCATGGT	CGTTAAAGCC	TTCCAACACT	CGGACGGTGC	GGCCTCCGCG	GACCACCTGA	240
GGAAACGCTG	GCTCCGGGAC	CGGGCGCGGG	GCTGCCAACA	CCCCACGATT	GAGATGGAAG	300
CGGATACGCC	GTGCGATGAC	ATCAGCGGAC	GCTCGATAGT	ACGCGCGCGC	GACACCGGCC	360
AGATCATGCT	TGAGCTCGGC	CAGCGGGGGG	TCGGTCCCGA	ACAGCGCCAG	CGGCGTGAAC	420
GGTGAGGCCA	GCATGCGCTG	CACCACCGAG	ACACCTTCGG	CGATCAGCAA	CGGCTTGCCG	480
GTGCGGAGAT	CGGGAACACN	GTGATGCTG	TTGAGCTCAC	GGAAATCGTC	GAGCGGTGGG	540
TCCTCGGGAT	CGCAGACGTC	GTGAACATCG	AGCGCTTCGG	GGTGTGCGGC	ACACCGGCTT	600
TGGGTTCGGT	GCTTTGCTCG	ACGAGAGGCA	GCATCAGATC	GGCGGCGCTG	CGCAGGATGT	660
CACGCTCGCT	GCGGTTTCAG	GTGCGGAGCC	GCTCAGCCAG	CGACTCTTCG	AGGAGGCGGT	720
TGCTGGGATT	AAATGGGAGA	GGAAACAGCC	ATGTCTTCGG	TGACCACACA	CGCGGAAGCC	780
CTGGCAGCTG	CGGCGCGGAA	CCTACAGGGT	ATTGCAACGA	CAATGAACGC	CGCGAAGCGG	840
GCGCGCGCTG	CTCGAACCCG	CGGAGTAGTG	CGCGCGCGCG	CGGATGAAGT	ATCAGCGCTG	900
ACCGGGGGCTC	AGTTTCTGTC	GCACCGCGAG	ATGTAGCAAA	CGGTGAGCGC	CGAGCGCGCG	960
GGCATCTCAG	AAATGTTGCT	GAACAGCGTG	GTGGCCAGTT	CTGGCTCATG	CGCGCGCACG	1020
GAGGCGGCCA	ACGCGAGCGC	TGGCGGCTGA	ACGCGCTCGC	ACGAACCTGC	TGAAGGAGAG	1080
GGGGAACATC	CGGAGTTCTC	GGGTACGGGG	TTGCGCCAGC	GGCGAGCCGA	TTCACTATATC	1140
GGGCTCCATA	ACAGCAGGAC	ATCTAGCCAT	TCACTACTAA	GGAGCAGGCG	AACATGGCTT	1200
CAGGTTTTAT	GACCGGATCG	CATGCGATGC	GGGACATGCG	GGCGGTTTTT	GAGGTGCGAG	1260
CGCAGACGGT	GGAGGACGAG	GCTCGCCCGA	TGTGGGCTGC	CGGCGCAAGC	ATTTCCGGTG	1320
CGGGCTGGAG	TGCGATGGCC	GAGCGGAGCT	CGCTAGAGAC	CATGACCTAG	ATGAATCAGG	1380
CGTTTCCGAA	CATCGTGAAC	ATGCTGCACG	GGGTGCGTGA	CGGGCTGGTT	CGCGACCCCA	1440
ACGAATACGA	CGACCAAGAG	CAGGCGCTGC	AGCAGATCTT	GAGCAGTAGT	CGCGGAAGCG	1500
CACAGCTGNG	TACGNTTTCT	CACATTAGGA	GAACACCAAT	ATGACGATTA	ATTACCGAGT	1560
CGGGGACGTC	GACGCTCAGT	GGCGGCTCAG	GGCGGCTCAG	GGCGGCTCAG	TTGAGCGCGA	1620
CAGCTACGGC	ATGATTCGTC	ATGATTCGTC	CGCGGCTGAC	TTTTGGGGGG	GGCGGCTGTC	1680
GGTGGCTTGC	CAGGAGTTCA	TTACCCGATT	GGGCGGTAA	TTGAGGTGA	TGACGAGGCA	1740
GG						1742

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2836 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGATTTGCG	TTGCGCGCGC	CGCGGAAGAC	CAACCACTGC	GCTGGGGTGG	TGGCACAGGC	60
GGTGTGCTCG	GTGAGCTGCG	CGAATCCCAA	TGATTTGGTG	CTCGGTTGCG	TTGCTGGGCT	120
CGATTACGCC	CACGGAAGAG	ACGACGATCG	TTGCTTTGCT	CGGTCAGTGC	TAGTTGGGGA	180
CGGCGATGGC	CGGGTTTCCT	ACCTCGATCG	CACAGCAGCT	GACCTTCGCG	CGAGGGGCGA	240
CAACGGCTGG	GTGCGCGCGA	GCTGTGTACC	CAAGGCCACA	ATTGCGCGCG	CTGGGTGCGG	300
GGCCGCGGGT	GTGCGCGGAT	TTGGCGCGCG	CGGAGCCGCT	CGGAGAGTTG	TCGGTTGCGG	360
CAAGTTGGGC	CGTGCGGCTT	CGGCGCTTGC	CGGAGAAAGC	TGAGGCGCGC	ACGCGGATGT	420
CGGTCATCGG	CGAAGCGCTG	AGCTCGCGTG	AGGAGGCGCT	GCTTCGAGTG	ATACGCGTGG	480
CGAGAGCGGG	CGGCGGTACA	GGCGGCTTGC	CTCACCGATA	CGGTTTCGCG	CACAGCGTGA	540
TTACCGCGTC	TGCGCGCGCG	GGATAGCTTT	CGATCGCGTC	TGCGCGCGCG	CGGAAATGCG	600
TGCAATAGGC	GATCGAGCCG	CGCGGTCGCT	AAACCGCGCA	CACGGCACTA	TCAATGCGCA	660
CGGCGCGCGT	TGATCCCAA	TTGACGCTCC	CGACGGGCGT	TTATCTCGCG	CAAGATTCCA	720
TCCCGAGCCC	GGTCCGTTGG	CGGATAAATA	CGCTGGTCCG	CGCGACTCTT	CGGCTGGAAT	780

TCGATGCTCT	GGGCGCCGCG	TCGACGCCGA	GTATCTCGAG	TGGGCCGCCAA	ACCGCGTCAA	840
ACGCTGTATC	TGTGCGGTTA	CCACAGGTGA	ATTTCGGGTG	CCAAGTGGTG	AACACTGTGG	900
AACGGGTGGC	ATCGAAATCA	ACTTGTTCGG	TTGCACTGAT	CTACTCTCTT	CGAGAGAGCC	960
GTTCGTGGGA	TYAATTTGGA	GAGGAGAGCA	GCATGTGCTT	CGTGACCAGA	CAGCGGGAGG	1020
CCCTGGCGAG	TGCGGCGGCG	AACCTACAGG	GTATTGGCAC	GACAAATGAAC	GGCCAGACCG	1080
CGCGCGCGCG	TGCTCCGAAC	ACCGGAGTAG	TGCCGCGCAG	CGCGGATGAA	GTATCAGGCG	1140
TGACGCGGCG	TCAGTTTCTT	GGCGACGCGC	AGATGTACCA	AACGGGTGAG	GGCCAGGCGG	1200
CGGCGATTCA	CGAAATGTTC	GTGACAGCGC	TGGTGCCGAG	TTCTGGCTCA	TACGCGGCCA	1260
CGGAGCGGCG	CAACGCGAGC	GCTGCGGCGT	GACGCGGCTC	GCACGAACCT	GCTGAGGAGG	1320
AGGGGGAGCA	TCGGAGTTTC	TCGGGTCAGG	GTTTGGCGCA	CGCGCCAGCC	GATTTCAGCTA	1380
TCGGCGTGCA	TAACAGCAGA	CGATCTAGCG	ATTCACTACT	AAGGAGACAG	CGAACATGCG	1440
CTCAGCTTTT	ATGACGGGATC	CGCATGCGAT	GGCGGACATG	CGCGGCGGTT	TTGAGGTGCA	1500
CGCGGAGAGC	GTGGAGGAGC	AGGCTGCGCG	GATGTGGGCG	TCGCGCGCAA	ACATTTCCGG	1560
TGCGGCGTGG	AGTGGCATGG	CGGAGCGGAC	CTCGCTAGAC	ACCATGACCT	AGATGAATCA	1620
GGCGTTTGGC	AACATCTGGA	ACATGCTGCA	CGGGGTGCGT	GACGGGCTGG	TTGCGGACGC	1680
CAACAACACT	GAACAGCAAG	AGCAGGCGTC	CCAGCAGATC	CTGAGCAGGT	AGCGCGGAAA	1740
GGCAGAGCTG	CGTACGCTTT	CTCAGATTAG	GAGAACAACA	ATATGACGAT	TAATTACCAAG	1800
TTGCGGGAGC	TCGACGCTCA	TGCGGCCATG	ATCGCGCTCT	AGCGCGCGTC	GCTTGAAGCG	1860
GAGCATCAGG	CCATCGTTTC	TGATGTGTTG	GGCGCGGGTG	ACTTTTGGGG	GGCGCGCGGT	1920
TCGGTGGCTT	GCCAGGAGTT	CATTACCCAG	TTGGGCGGTA	ACTTCCAGGT	GATCTACGAG	1980
AGCGCGCAAG	CCCACGGGCA	GAGGTTGAG	GCTGCCGGCA	ACAACATGCG	CGAAACCGAC	2040
AGCGCGCTCG	GCTCGAGCTG	GGCTTAAAC	TGAATTTGAG	TGCGCGCAGC	AGACCAACCA	2100
CGCGGTGTGC	TGCGGTGTGC	TGCAGTTAAC	TAGCACTCGA	CGCTGAGGT	AGCGATGGAT	2160
CAACAGAGTA	CCGCGACCGA	CATCAGCTCT	AACTGCGAG	GCTTCTGGAT	GCTTCAGGCG	2220
CTACTGGATA	TCGCGACGCT	TGCGGCTGAG	TTACGTTGCC	GGCGGTACCT	CTCCACCGAT	2280
TGCAATGACT	GGCTTAAACGA	GCACCGGAGG	ATGCGGGTCA	TGCGCGGAGCA	GGCGATTGTC	2340
GTCAACAGAG	CGGTCAACGA	ACAGGTGCGT	GGCGGATGA	AGGTGCTTGC	CGACACTGAT	2400
CTTGAAGTGC	TGCGGCTGCT	CTCAGCGGCG	AGTGTGCTGT	ACGGGTGCTAT	AGACGAGGAG	2460
AAACAGCGCG	CGGCTTGGCG	TGACATGCGT	GACAAATGAG	TGCGGGTGGT	GTTGGCGCGG	2520
CGAGGCGAGC	ACTGGGTGTC	GGCGGTACGG	GTTGGCAATG	ACATCACCGT	CGATGACGTG	2580
ACGGTCTCGG	ATAGGCGCTC	GATCGCGGCA	CTGGTAAATG	ACGGTCTGGA	GTGGAATTAC	2640
CACGCGGAGC	CACCGCGGAT	CAACGCGGTC	AACTGTGCAA	TGGAGGAGAT	CTGTGCGCGA	2700
ATTGCGGACG	AGGACAGAGG	CGGTGTGCGT	GACGACGGGA	TGATCATCGA	TCATCGACCG	2760
GCGCGGATCC	TGGCGGATCT	GTTGAGCAC	GACCGCGGCG	CGCGGGAAGC	TCTGCGACAT	2820
CGATGGGTTT	TTCCGG					2880

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Thr	Ile	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met
1			5					10					15		
Ile	Arg	Ala	Leu	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile
			20					25					30		
Ser	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala
			35					40					45		

Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
 50 55 60
 Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
 65 70 75 80
 Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
 85 90

Mtb9.9A (MTI-A) ORF peptides

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
1 5 10 15

{2} INFORMATION FOR SEQ ID NO:54:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(v1) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(x) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Mer 11e Aeg Ala Gin Ala Ala Ser Iau Glu Ala Glu His Gin Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:55:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Ala Ser Leu Glu Ala Glu His Gin Ala Ile Val Arg Asp Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Glu His Gln Ala Ile Val Arg Asp Val Leu Ala Ala Gly Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ile Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly	Ser	Val	Ala	Cys	Gln	Glu	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln	Glu	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu
1					5				10					15	
Gln	Ala														

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu	Gln	Ala	Asn	Ala	His	Gly	Gln
1					5				10					15

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile	Tyr	Gla	Gln	Ala	Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala	Gln	Thr	Asp	Ser	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
 1 5 10 15

Mtb9.8 (MSL)

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 585 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGGATTCCGA	TAGCGTTTC	GGCCCTCGA	CGGCGACCA	CGGCGGCGAG	GCCTCCGAAC	60
GGGGGGCCCG	GAGCTGGGA	TTGCGCCGGA	CGGCAACCA	AGAACCCTCG	GTCCGCGCG	120
TGGGGCTGAC	CGCACTGGCC	GATGATGAT	TGGGCAACG	CCCCCGGATG	CGATGCTGC	180
CGGGGACCTG	GGAGCAGGG	AGCAAGAGG	CGAGGCGGCC	CGACGGATG	GGAGAGGGG	240
GAGGCGACCG	CTTACCGAC	GACAGCAAGT	AACCGAATC	CGAATCACGT	GGACCCGTAC	300
GGGTGGAAAG	GAGAGATGT	ATGAGCTTT	TGGATGCTCA	TATCCACAG	TTGTTGGCT	360
CCCATGCGGC	GTTTCCCGCC	AAAGCGGGGC	TGATCGGCA	CAGATCGGT	CAGGCGGAGC	420
AGGCGGCGAT	GTGCGCTCAG	CGTTTTCACC	AGGGGAGTC	GTGCGGCGCG	TTTCAAGCCG	480
CCCATGCGCG	GTTTGTGCGC	CGGCGCGCCA	AAGTCAACAC	CTTGTGTGAT	GTGCGGCGAG	540
CGAATCTGGG	TGAGCGCGCC	GATACCTATG	TGGCGGCGGA	TGCTG		585

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met	Ser	Leu	Leu	Asp	Ala	His	Ile	Pro	Gln	Leu	Val	Ala	Ser	Gln	Ser
1				5				10				15			
Ala	Phe	Ala	Ala	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala
				20				25				30			
Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser

[illegible]

Mtb9.8 ORF peptides

(2) INFORMATION FOR SEQ ID NO:110:

(4) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:111:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
1 5 10 15

{2} INFORMATION FOR SEQ ID NO:112:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: peptide

(k1) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
2 5 10 15

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Ser	Ala	Phe	Ala	Ala	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln
1					5					10				15

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gln	Ala	Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

15

2

5

10

15

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu Leu Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala
 1 5 10 15
 Asp Ala

Mtb39A (TbH9)

(2) INFORMATION FOR SEQ ID NO:106:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCGTACCC	GTCCGAGTCC	TCCGCGCCGT	TTAGGATGGA	GTGACAGTGT	CTTTCGTUAT	60
GGCATAACCA	GAGATGTTGG	CGCGCGCCGC	TTACACCCCTG	CAGAGCATCG	GTGCTACACAC	120
TGTGCTAGC	AATGCCGCTG	CGCGCGCCGC	GACGACTGGG	GTGCTGCCGC	CGGCTGCCGA	180
TGAGGTGTGG	CGGCTGACTG	CGCGCGCACTT	CGCGCACAT	CGCGCGATGT	ATCAGTCCGT	240
GAGCGCTCGG	GCTGCTCGGA	TTCATGACCA	GTTCGTGGCC	ACCGTTGGCA	GCAGCGCCAG	300
CTCCTATGCG	GCCACTGAAG	TGGCAATGCG	GGCGCGCGGC	AGCTAAGCCA	GGACAGTGG	360
GCACAGAGAA	CTACAGAGAA	TAGGACACCG	TAATGCTGGA	TTTCGGGGGG	TTACCAACCG	420
AGATCAACTC	CGCGAGAGAT	TACGCGCGCC	CGGCTTCGGC	CTCGCTGGTG	CGCGCGCGCTC	480
AGATGTGGGA	CAGCGTGGCG	AGTGACCTGT	TTTCGGCGCG	GTGCGCGCTT	CAGTCCGTGG	540
TCTGGGCTCT	AGATGTGGGG	TGCTGGATAG	GTTCGTGGCG	GGGTCTGATG	GTGCGCGCGCG	600
CCTCGCGCTA	TGTGGCTGTG	ATGAGCTGCA	CGCGCGCGCA	GGCGAGCTG	ACCGCGCGCC	660
AGGTCCGGGT	TGCTCGCGCG	GCTTACGAGA	CGCGCTATGG	GCTGACGGTG	CGCGCGCGCG	720
TGATCCCGGA	GAACCTGCT	AACGAGCGCG	AATACCGGGA	GATGTGGGGC	CAAGACCGCC	780
ACACCCCGGC	GATCGCGTTC	AACGAGCGCG	CGACCGCGAC	GGCGAGCTTG	CTGCGCTTCG	840
CGCGGATGTT	TGGCTACGCT	CGCGCGCGCG	CGACCGCGAC	GCAGCGCGCG	CGCGGTGAGG	900
AGGAGCGCGC	GGAGATGACC	ACCGCGCGGTG	GGCTCTCGGA	GCAGCGCGCG	CGCGGTGAGG	960
AGGCTCTCGA	CACCGCGCGG	CGCAACCAAT	TGATGAACAA	TGTGCCCGAG	GGCGCTGAC	1020
AGCTGCCCCA	CGCCACCGAG	GGCAACCAAC	CTTCTTCCAA	GCTGGGTGGC	CTGTGGAAGA	1080
CGCTGCTCGC	GCATCGGTGG	CGGATGACCA	ACATGCTGTC	GATGGCGCAAC	AACGACATGT	1140
CGATGACCAA	CTCGGCTGTT	TGATGACCA	ACACCTTGAG	CTCGATGTTG	AGGGGCTTTG	1200
CTCGCGCGCG	GGCGCGCGCG	CGCTTCCAAA	CGCGCGCGCA	AAACCGGGGT	CGCGCGATGA	1260
GCTCGCTGGG	CAGCTCGGCT	GTTTCTTCGG	GTCTGGCGCG	TGGGGTGGCG	GCCAACTTGG	1320
GTGCGCGCGC	CTCGGTGGGT	TGTTTCTCGG	TGCGCGCGCG	CTGGCGCGCG	GCCCAACCGG	1380
CAGTCAACCC	GGCGCGCGCG	GGCTTCCCGG	TGACCAAGCT	GACCAAGCGC	GGCGAAGAGG	1440
GGCGCGCGCA	GATGCTGGCG	TGGCTGCGCT	TGGCGGAGT	GGCGCGCGCG	GGCGGTGGTG	1500
GGCTCAAGTG	TGTGCTGCGT	GTTCGCGCGC	GACCTATGTT	GATCGCGCAT	TCTCGCGCGG	1560
CGCGCTAGGA	GAGGGGGCGC	AGACTGTGCT	TATTGACCA	GTTTACAGGA	TTAGGTCAG	1620
TTCGCGCGCG	CGCTATGACA	ACAGTCAATG	TGATGACAA	GTTTACAGGA	TTAGGTCAG	1680
GTTCACCAAG	GAGACAGGCA	ACATGGCGCT	ACGTTTATG	ACGGATCGCG	ACCGGATGCG	1740
GGACATCGCG	GGCGCTTTTG	AGGTGCAACG	CGAGACGGTG	GAGGACGAGG	CTCGCGGAT	1800
GTGGCGCTGC	CGCGAAAACA	TTTCGGGTGC	GGGCTGGAGT	GGCATCGCGG	AGGCGACCTC	1860
GCTAGACACC	ATGGCCGAGA	TGAATCAGCG	GTTCGCAAC	ATCTGGAACA	GTCTGCAACG	1920
GGTGGGTGAC	GGGCTGGTGT	GCGACGCCAA	CAACTACGAG	CAGCAGAGAG	AGGCTTCCCA	1980
GCAGATCTCT	AGCGCTTAC	GTACGCGCT	GCAGCAGAT	ACTTTTACAA	CGGAAAGGGA	2040
ACAGGTTTGA	TGACCATCAA	CTATCAATTC	GGGATGTCG	ACGCTACAGG	CGCATGATGT	2100
CGCGCTCAGG	CGCGGTGCT	GGAGGCGGAG	CATCAGGCCA	TCAATCGTGA	TGTGTGACCC	2160
CGGAGTGACT	TTTGGGCGCG	CGCGGTTGCG	GGCGCTGCG	AGGGGTGCT	TACCCAGTTG	2220

GGCCGTAAGT	TCCAGGTGAT	CTACGAGCAG	GCCACGCCCC	ACGGGCGAGAA	GGTGCAAGCT	2230
GGCCGCAACA	ACATGGCGCA	AACCGACAGC	GGCGTCGGCT	CCAGCTGGGC	CTGACACCAAG	2340
GGCAAGGCCA	GCGACGTGGT	GTACAGATGA	AGTTCTCTGC	GTGATCTCTC	GGGTGGCAAT	2400
CTAAGTGTTC	AGTCTGGGGG	TGTTGGTGGT	TTGCTGCTTG	GCGGTTCTTT	CGGTGCTGGT	2460
CAGTCTGCTG	CGGCTCTGGG	TGAGGACCTC	GAGGCCCGAG	TAGCGCCGTC	CTTGGATCCA	2520
TTGCTGCTGT	TGTTGCGGCA	GGACGGCTCC	GACGAGGCGG	ATGATCGAGG	CGCGGTCTGG	2580
GAAGATGCCC	ACGAGCTCGG	TTGCGGCTCG	TACCTCTCGG	TTGAGGCGTT	CCTGCGGGTT	2640
GTTGGACCAAG	ATTTCGCGCC	AGATCTGCTT	GGGGAAGCGG	GTGAACGCCA	CGAGGTCTGG	2700
CGCGGCGGTT	TGGAGGTGCT	CGGCGACCGC	GGGAGGTTTG	TGGGTCAGAG	CGTCAAGTAC	2760
CGGATCATAT	TGGGCAACAA	CTGATTCTGG	GTGCGGCTGG	TCTTAGATGG	AGTCCAGCAG	2820
GGTGCGCACC	CACGCGCAGG	AGGCGTTCTG	GTTGGCTGCC	ATCAGATTGG	CTGCGTAGTG	2880
GTTTCTGCAG	CGCTGCGAGG	CGGCTGCGGG	CAGGCTGGGG	CGGATCGCGG	CCACCAAGGC	2940
GGCGTGGGCG	TGCTGTGTGA	CCAGCGCGAC	GGCGACAGG	CGCGGGCGCA	CCAGGTCTGG	3000
GAAGAACGCC	AGCCAGCCGG	CGCGGTCCTC	GGCGAGGTTG	ACCTGGATGC	CCAGGATC	3058

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met	Val	Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met
1				5					10					15	
Tyr	Ala	Gly	Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp
			20					25					30		
Asp	Ser	Val	Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser
		35					40					45			
Val	Val	Trp	Gly	Leu	Thr	Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly
		50				55				60					
Leu	Met	Val	Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr
	65				70				75					80	
Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala
		85							90				95		
Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala
		100							105				110		
Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly
		115					120					125			
Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met
		130				135					140				
Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala
	145					150			155					160	
Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr
				165					170				175		

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Val Glu Glu Ala Ser
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380
 Pro His Ser Pro Ala Ala Gly
 385 390

Mtb32A (TbRa35)

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTTG GGTAGAGAAA ATCTCTCCGC CGGACCCCTT AAGGCTGGGA CAATTTCGTA

TAGCTACCCC GACACAGGAG GTTACGGGAT GAGCAATTGG CGCCGCCGCT CACTCAGGTG 120
 GTCACTGGTTG GTGAGCGGTG CTGGCTGGGG CTGGCCACGG CGCCGCCGCA 180
 GCGCGCCCGG CGCGCCCTGT GTGAGGAGGT GTTCCCGGAC TTCCCGCGCG TCGCCCTCGA 240
 CCGCTCCCGG ATGCTCGCCC AAGTGGCGCC ACAGGTGGTC AACATCAACA CCAAACTGGG 300
 CTACAAACAAC GCGCTGGCGG CGCGGCCGAC CGACATCAAT GCGTTCCAGG TCGGCTCCGG 420
 CCAAACTGAT GCGCTGGATG TGGTGGGTTA TGACCGCAAC CAGGATGTGG GGTGCTGGA 480
 GCTGCGCGGT GCGCTGGCGC TCGCTGGCGG GCGGATCGGT GCGCGCGTGG CGGTGGTGA 540
 GCGCTCGCTG GCGATGGGCA ACAGCGGTGG CGAGGGCGGA ACGCCCTGTT GGTGGCTGG 600
 CAGGGTGGTG GCGCTGGCGC AAGCGTGGCA GCGCTGGAT TCGTGAACG GTCCCGAAGA 660
 GACATGGAAC GGGTGGATCC AGTTCGATGC CGCAATCCAG CCGCTGATT CGCGCGCGCC 720
 CGTCTGCAAC GCGCTAGGAC AGGTGGTGGG TATGAACAG CGCGCGTGG ATAACTTCCA 780
 GCTGTCCGAG GGTGGCGAGG GATTCGCCAT TCGATCGGG CAGCGGATGG CGATCGCGGG 840
 CCAAACTGGA TCGGTGGGG GGTCAACCGC GTTCATATC GCGCTTACGG GCTTCTCGG 900
 CTTGGGTGTT GTGACAAACA ACAGCAACGG CGCACGATC CAACCGTGG TCGGAAGCGC 960
 TCGCGCGGCA AGTCTCGGCA TCTCCACCGG CGACGTGATC AGCGCGGTGG ACAGCGCTCC 1020
 GATCACTGCG GCGACCGGGA TCGCGGACGG GCTTAAACGG CATCACTCGG GTGACGTGAT 1080
 CTCGTTGAAC TGGCAAAACA AGTGGCGCGG CAGCGGTACA GGGAACTGGA CATTTGCGGA 1140
 GCGACCCCGG GCGTGAATTG TCGCGGATAC CAGCGCGCGG CGCGCGCAAT GGATTGGCGC 1200
 CAGCGGTGAT TCGCGCGTGA GCGCGCGGAT TCGCTCTCGG GTCGCGGTGG CATTTGCGGA 1260
 GCAATGAACG AGCGAGAACA CAGCGTTGAG CAGCTCTCGG TCGAGCGGAG TTACTGCGAA 1320
 GCGCGGTGGG TCGCGGATCC GATTCGCGGA GACTTCGGGA CGCGCGCGCG GTGCGCGCGC 1380
 GATCCGACCT GGTTTAGCA CCGCTCTTTC TAGAGGTGG TGGTCCGGGG GTTCTTCGAC 1440
 GCGAGCGCGG AGCGTTCGCG GATCTCGGT GACTCTAGG ACTCAGCGCT GCGCGAGCGC 1500
 TGGCTTGGGA TCGACTGCAT CTCTTCGCGC GGTTCCTAGG ACTCAGCGCT GCGCGAGCGC 1560
 GGTTCAGCA TTGCGGACTT CTACAGGTTG CTGCGCGAAT TCGCGAGCGT CGACGATTTT 1620
 GTGCGCGTGG TCGACACCGG TCACCGCGGA GGTATCCGGA TCATCAGCGA CCTGGTGATG 1680
 AATCAGACCT CGAGTTCGCA CCGCTGGTTT CAGGAGTCCC GCGCGGACCC AGACGAGCGC 1740
 TACGTTGACT ATTAGTGTG GAGCGACACG AGGAGCGGCT ACACCGAGCC CGGATCATC 1800
 TTCGTGCA CCGAAGGATC GAATCTGCA TTGATCTGTT TCGCGCGACA GTTCTACTG 1860
 GCACCGATTG TT

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
 1 5 10 15
 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 20 25 30
 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala

115	120	125
Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly		
130	135	140
Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly		
145	150	155
Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu		
160	165	170
Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Gln Thr		
175	180	185
Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser		
190	195	200
Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr		
205	210	215
Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala		
220	225	230
Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly		
235	240	245
Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu		
250	255	260
Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val		
265	270	275
Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile		
280	285	290
Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp		
295	300	305
Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln		
310	315	320
Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly		
325	330	335
Pro Pro Ala		
340	345	350
355		

Mtb8.4 (DPV)

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CGTGGCAATG TCGTTGACGG TCGGGGCGGG GGTGGCTGCG CGAGATCCCG TGGACGGGTT	60
CATTACACACC ACCTGCAATG ACGGGCGAGT AGTAGGCTGCG CTCACGGCGA CGGATCCGGG	120
GGTGGCGGCA CAGTTGAAAG CCGTACCGGT GCGCGAGTCC TATTTGCGCA ATTTCCTGCG	180
CGCACGGCCA CCGCAGGGCG CTGCGCATGGC CGCGCAATTG CAAGCTGTGC CGGGGGCGGG	240
ACAGTACATC GGCCTGTGCG AGTCGGTTGC GGGCTCTGCG AACCACTATT AAGCCCATGCG	300
GGGCCCGATC CGCGCAGCCG GCACTGCTGC GGGGCTTAGG CCAGATTGCG CCGCTCCTCA	360
ACGGGGCGCA TCGGCGGACC CGGCTGCTGC GCGCGGGCTA GCGCAGATTG GCGCGGCTCT	420
CAACGGGGCG CATCTGTGCG CGAATCTCTG CAGCGCGGGG GATCCACTAG TTCTAGAGCG	480
GGCGCCACCG CGGTGGAGCT	500

(2) INFORMATION FOR SEQ ID NO:102:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x4) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Val	Ala	Met	Ser	Leu	Thr	Val	Gly	Ala	Gly	Val	Ala	Ser	Ala	Asp	Pro
1			5						10					15	
Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala
		20						25					30		
Ala	Leu	Asn	Ala	Thr	Asp	Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser
	35					40						45			
Pro	Val	Ala	Gln	Ser	Tyr	Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro
	50				55					60					
Gln	Arg	Ala	Ala	Met	Ala	Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala
65			70					75						80	
Gln	Tyr	Ile	Gly	Leu	Val	Glu	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr
			85					90						95	

Meib11 (Tb38-1)

(2) INFORMATION FOR SEQ ID NO:46:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGCGCAGGAG	GACCGATGCC	GCTACCTCG	CGCAGGAGGC	AGGTAATTTC	GAGCGGATCT	69
CGCGCGACCT	GAAGAACCCG	ATCGACACAG	TGGATCTGAC	GGCAGGTTTC	CGACGAGGCC	120
AGTCGCGCGG	CGCGCGGGGG	AGCGCGCGGT	GCTGGCGGTC	CAAGAAGACG	138	
CCAAATGACG	GAAACAGGAA	CTCGACAGAA	TCTCGACGAA	TATTGGTTCG	GCGGCGCTCC	240
AATACTCGAG	GGCGGACGAG	GAGCAGCAGC	AGGCGCTGTC	CTCGCAAAAT	GCGCTTCTGC	300
CCGCTAATAC	GAAGAGAAAC	GGAGCAA				327

(2) INFORMATION FOR SEQ ID NO:58:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
1 5 10 15
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly

[illegible]

TbRa3

(2) INFORMATION FOR SEQ ID NO:15:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(x4) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTGGCGCA	CGAGAGTGA	TGACATCAT	CGAGACGAGC	CGACATCGCT	GGGACGAGG	60
CGGCGCGAG	CGCGTCCAGC	CGGCGCGGGA	TAGCGTCCAT	GACATCCCGT	TCGTCGGGT	120
CATCGCGAG	GACATCGGCG	TGACAGCGG	CGGCAAGATC	CGATTACCGCA	TCAAGTCTGA	180
AGTGTCTCTT	AGATAGCGC	CGGCGCAACG	CGGCTAGCAC	GAGCGCGGGA	GCAGAGCGCA	240
AAATCGCGCA	GTTCGCGGT	GATTCGTGCG	ATTTTGTGTC	TGCTCCGCGA	GCGCTACGAG	300
CGGCGCGCCA	GGTCCGCGTG	CTGCGGTATC	CGGCGGTGCA	TGCGGATTGC	GCGGCGCGAG	360
CGCGGATTA	TGCTTCGCGT	CGACCGAAC	TGGCGGATCC	CGCGGNGGCA	TGATCGATGA	420
CGTGTGCGAC	CGGCTCGATG	CGGAGTTTC	CGGAGGAAAC	GTGCTGCCAG	GCGGTATAGA	480
AGCGTCCGTA	GCGCGCGGTG	CTGACCGGCT	CTGCTTGCGC	CTTCAGTCCG	GCCAGCGAGC	540
GG						542

(2) INFORMATION FOR SEQ ID NO: 77:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
1 5 10 15
Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
20 25 30
Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
35 40 45
Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
50 55 60
Pro Arg
65

38kD

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTTCTTGA	CGGCGGGCTG	TGCGAGGAAG	GGCCACCGGA	ACAGCTGTTG	TCGTCGGCGA	40
AGCATGCGGA	AACGCGCGGA	TACGTGCGCG	GACTGTGCGG	GGAGCTCAAG	GACGCGCAAGC	120
CGCGAAATTG	AAGAGCACAG	AAAGGTATGG	CGTGAAUATT	CGTTTGATCA	CGCTGTTGGC	180
GCTTTTGACC	GCTGCGCGCG	TGCTGCTAGC	AGCGCGCGCG	TGTGGCTCGA	AAGCACCGAG	240
CGGTTTGGCT	GAAACGGGCG	CGGCGCGCGG	TACTGTGCGG	ACTACCCCGG	CGTGTGCGCC	300
GGTGAGCGTG	GCGGAGACCG	GTAGCACGCT	GCTCTACCGG	CTGTTCAACC	TGTGGGGTCC	360
GGCCTTTTCA	GAGAGGTTAT	CGAACCTCAC	GATCACCGGT	CAGGCGACGG	GTTCTGGTGC	420
CGGATTCGCG	CAGGCGCGCG	CGGGAGCGGT	CAACATTGGG	GGCTCCGACG	CGTATCTGTC	480
GGAAAGTGAT	ATGGCGCGCG	ACAAAGGGCT	GATGAACATC	GGGCTAGCCA	TCTCGCTCA	540
CGAGGTCAAC	TACCAACTGC	CCGAGTGTAG	CGAGCACCTC	AAGCTGAACG	GAATAATCTC	600
GGCGGCGCAT	TACCAAGGCA	CCATCAAAGC	CTGGGACGAC	CGCGAGATCG	CTGGCGCTCA	660
CGCGGGGCTG	AAGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CACCGCTCCG	ACGGGTCGCG	720
TGACACCTTC	TGTTTTCAGC	AGTACCTGTC	CAAGCAAGAT	CGCGAGGGCT	GGGGGAAGTC	780
CGCCGGGCTG	AGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CGCGAGGGCT	GGGGGAAGTC	840
TGACACCTTC	TGTTTTCAGC	AGTACCTGTC	CAAGCAAGAT	CGCGAGGGCT	GGGGGAAGTC	900
CGCCGGGCTG	AAGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CGCGAGGGCT	GGGGGAAGTC	960
TGACACCTTC	TGTTTTCAGC	AGTACCTGTC	CAAGCAAGAT	CGCGAGGGCT	GGGGGAAGTC	1020
CGCCGGGCTG	AAGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CGCGAGGGCT	GGGGGAAGTC	1080
TGACACCTTC	TGTTTTCAGC	AGTACCTGTC	CAAGCAAGAT	CGCGAGGGCT	GGGGGAAGTC	1140
CGCCGGGCTG	AAGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CGCGAGGGCT	GGGGGAAGTC	1200
TGACACCTTC	TGTTTTCAGC	AGTACCTGTC	CAAGCAAGAT	CGCGAGGGCT	GGGGGAAGTC	1260
CGCCGGGCTG	AAGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CGCGAGGGCT	GGGGGAAGTC	1320
TGACACCTTC	TGTTTTCAGC	AGTACCTGTC	CAAGCAAGAT	CGCGAGGGCT	GGGGGAAGTC	1380
CGCCGGGCTG	AAGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CGCGAGGGCT	GGGGGAAGTC	1440
TGACACCTTC	TGTTTTCAGC	AGTACCTGTC	CAAGCAAGAT	CGCGAGGGCT	GGGGGAAGTC	1500
CGCCGGGCTG	AAGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CGCGAGGGCT	GGGGGAAGTC	1560
TGACACCTTC	TGTTTTCAGC	AGTACCTGTC	CAAGCAAGAT	CGCGAGGGCT	GGGGGAAGTC	1620
CGCCGGGCTG	AAGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CGCGAGGGCT	GGGGGAAGTC	1680
TGACACCTTC	TGTTTTCAGC	AGTACCTGTC	CAAGCAAGAT	CGCGAGGGCT	GGGGGAAGTC	1740
CGCCGGGCTG	AAGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CGCGAGGGCT	GGGGGAAGTC	1800
TGACACCTTC	TGTTTTCAGC	AGTACCTGTC	CAAGCAAGAT	CGCGAGGGCT	GGGGGAAGTC	1860
CGCCGGGCTG	AAGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CGCGAGGGCT	GGGGGAAGTC	1920
TGACACCTTC	TGTTTTCAGC	AGTACCTGTC	CAAGCAAGAT	CGCGAGGGCT	GGGGGAAGTC	1980
CGCCGGGCTG	AAGCTGCGCG	GCACCGCGGT	AGTTCCGCTG	CGCGAGGGCT	GGGGGAAGTC	1993

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
1 5 10 15

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
20 25 30

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
35 40 45

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
50 55 60

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
65 70 75 80

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
85 90 95

Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
100 105 110

Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
115 120 125

Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
130 135 140

Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
145 150 155 160

Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
165 170 175

Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
180 185 190

Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
195 200 205

Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
210 215 220

Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
225 230 235 240

Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
245 250 255

Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
260 265 270

Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
275 280 285

Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
290 295 300

Ala	Pro	Asp	Gly	Tyr	Pro	Ile	Ile	Asn	Tyr	Glu	Tyr	Ala	Ile	Val	Asn
305					310				315					320	
Asn	Arg	Gln	Lys	Asp	Ala	Ala	Thr	Ala	Gln	Thr	Leu	Gln	Ala	Phe	Leu
			325						330					335	
His	Trp	Ala	Ile	Thr	Asp	Gly	Asn	Lys	Ala	Ser	Phe	Leu	Asp	Gln	Val
			340					345					350		
His	Phe	Gln	Pro	Leu	Pro	Pro	Ala	Val	Val	Lys	Leu	Ser	Asp	Ala	Leu
			355				360						365		
Ile	Ala	Thr	Ile	Ser	Ser										
			370												

DPEP

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 999 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACC	ATCACCATCA	CATGCATCAG	GTGGACCCCA	ACTTGACACG	TGGCAAGGGA	60
CGATTGGCGG	CACATGGCTAT	CCGCGCGATG	GCGAGCGCCA	GCGTGGTGAC	CGTTGGGCTG	120
CCCGCGACCG	CCACGCGCGA	TCCGAGGCCA	GCGCCCCCGG	TACCCACAAC	GCGCGCCTCG	180
CCGCGGTGGA	CGGCTGCAAC	GCCACCCGCA	CGGCGGACAC	CTGTTGCCCC	CCCACCAACG	240
GCGCGCGCCA	ACAGCGCGAA	TGCCAGCCG	GCGCATCCCA	ACCCAGCACG	TCCGCGCGCC	300
GACCCGAACG	CACCGCGCGC	ACCTGTCAAT	GCCCCAAGC	CACCCCAACG	TGTCCGGATC	360
GACAAACCGG	TTGGAGGATT	CAGCTTCGCG	CTGCTGCTG	GCTGGGTGGA	GTCTGACGCC	420
GCCCACTTCG	ACTACGGTTC	AGCACTGCTC	AGCAAAAGCA	CGGGGAGCCC	GCAATTTGCC	480
GACACGCGCG	CGCCGCTGCG	CAATGACACG	CGTATGCTG	TCCGCCCGCT	AGACCAAAAG	540
CTTTACGCGA	GCGCGGAAGC	CACCGACTCC	AAGGCGCGCG	CCCGGTTGGG	CTGGGACATG	600
GCTGAGTTCT	ATATGCCCTA	CCCGGGCAAC	CGGATCAACC	AGGAAACCGT	CTCGCTCGAC	660
GCCAAACGGG	TGCTCGGAAG	CGCTGCTAT	TACCAAGTCA	AGTTCAAGCA	TCCGAGTAAG	720
CGGAACGGCG	AGATCTGGAC	GCGCTAATC	GCTCGGCGCG	CGGCGAAGCG	ACCGGACGCG	780
GCGGCGCGCT	AGCGCTGCTT	TGCTGATGCG	CTCGGGAACG	CCAACAACCC	GCTGGACACG	840
GCGCGCGCCA	AGGCGCTGCG	CGAATCGATC	CGCGCTTTGG	TGCGCCCGCC	GCGCGCGCGG	900
GCAACGCGCT	CTGCAGAGCC	CGCTCGCGCG	CCGCGCGCGG	CCGCGGAAGT	CGCTCTTACC	960
CGACGACAC	CGACACCGCA	GCGGACTTTA	CCGCGCTGGA			999

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

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Met His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1      3      10      15
Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20      25      30
Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35      40      45
Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50      55      60
Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65      70      75      80
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85      90      95
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100      105      110
Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
115      120      125
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
130      135      140
Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145      150      155
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
160      165      170      175
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
180      185      190
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
195      200      205
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
210      215      220
Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
225      230      235      240
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
245      250      255
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
260      265      270
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
275      280      285
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
290      295      300
Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
305      310      315      320
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
325      330

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TbH4

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 702 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCC ATTGCGCCGGG TTCCGCCACC

CGAGGAAAGC	CGCTACGAGA	TGGCGCTGCC	GAAGTAGGGC	GATCCGTTCC	CGATGCCGGC	120
ATGAACGGGC	GGCATCAAAAT	TAOTGCAGGA	ACCTTTCACT	TTAGCCGACGA	TAATGGCTAT	130
AGCACTAAGG	AGGATGATCC	GATATGACCC	AGTCCGAGAC	CCTGACGGTG	GATCAGCAAG	240
AGATTTTGAA	CAGGCGCAAC	GAGGTGGAGG	CCCGGATGGC	GGAACCCAGC	ACTGATGTCC	300
CCATCAGACC	GTGCGAACTC	ACGGGCGGTA	AAAACGCCGC	CGAACAGNTG	GNTTGTCCCG	360
CGGACAACAT	CGCGGAATAC	CTCGCGGCGC	GTGCGCAAGA	CGCGGCGCGT	CTGCGCGACCT	420
CGCTCGCGAA	CGCGCGCAAG	GNGTATGCGC	AGGTTGATGA	CGAGGCTCGC	ACCGCGCTGG	480
ACAACGACGG	CGAAGGAACAT	GTGCGAGCAG	AATCGGCGCG	GGCGGTGGGA	GGGGACAGTT	540
CGCGCGAATC	AACCGATACG	CGGAGGCTGG	CCACGGCGCG	TGAACCCCAAC	TTGATGGATC	600
TCAAGAAGAC	CGCAAGGAAG	CTCGAAACCG	CGCACCAAGG	CGCATCCCTC	CGGCACTGNG	660
GGGATGGGTC	CAACACTTNC	ACCTTGACGC	TGCAAGCGCA	CG		702

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly	Asp	Ser	Phe	Trp	Ala	Ala	Ala	Asp	Gln	Met	Ala	Arg	Gly	Phe	Val
1				5					10					15	
Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Thr	Gly	Glu	Gly	Leu	Gln
			20					25						30	
His	Ala	Asp	Gly	His	Ser	Leu	Leu	Leu	Asp	Ala	Thr	Asn	Pro	Ala	Val
			35					40						45	
Val	Ala	Tyr	Asp	Pro	Ala	Phe	Ala	Tyr	Glu	Ile	Gly	Tyr	Ile	Asa	Glu
		50				55					60				
Ser	Gly	Leu	Ala	Arg	Met	Cys	Gly	Glu	Asn	Pro	Glu	Asn	Ile	Phe	Phe
						70					75			80	
Tyr	Ile	Thr	Val	Tyr	Asn	Glu	Pro	Tyr	Val	Gln	Pro	Pro	Glu	Pro	Glu
			85					90						95	
Asn	Phe	Asp	Pro	Glu	Gly	Val	Leu	Gly	Gly	Ile	Tyr	Arg	Tyr	His	Ala
			100					105						110	
Ala	Thr	Glu	Gln	Arg	Thr	Asn	Lys	Xaa	Gln	Ile	Leu	Ala	Ser	Gly	Val
			115				120							125	
Ala	Met	Pro	Ala	Ala	Leu	Arg	Ala	Ala	Gln	Met	Leu	Ala	Ala	Glu	Trp
			130			135						140			
Asp	Val	Ala	Ala	Asp	Val	Trp	Ser	Val	Thr	Ser	Trp	Gly	Glu	Leu	Asn
						150					155			160	
Arg	Asp	Gly	Val	Val	Ile	Glu	Thr	Glu	Lys	Leu	Arg	His	Pro	Asp	Arg
						165					170			175	
Pro	Ala	Gly	Val	Pro	Tyr	Val	Thr	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Gly
						180								190	
Pro	Val	Ile	Ala	Val	Ser	Asp	Trp	Met	Arg	Ala	Val	Pro	Glu	Gln	Ile
						195								205	
Arg	Pro	Trp	Val	Pro	Gly	Thr	Tyr	Leu	Thr	Leu	Gly	Thr	Asp	Gly	Phe
						210								220	
Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Gly	Arg	Arg	Tyr	Phe	Asn	Thr	Asp
						225								240	
Ala	Glu	Ser	Gln	Val	Gly	Arg	Gly	Phe	Gly	Arg	Gly	Trp	Pro	Gly	Arg
						245					250			255	
Arg	Val	Asn	Ile	Asp	Pro	Phe	Gly	Ala	Gly	Arg	Gly	Pro	Pro	Ala	Gln
						260					265			270	
Leu	Pro	Gly	Phe	Asp	Glu	Gly	Gly	Gly	Leu	Arg	Pro	Xaa	Lys		

275

280

285

MTbRa12

(2) INFORMATION FOR SEQ ID NO:4:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

CGGTATGAAC ACGGCGCGCT CGGATAACTT CCAGCTGTCC CAGCGTGGGC AGGGATTCCG      60
GATTCCGATC GGGCAGGCGA TGGCGATGCG GGGCCAGATC CGATCGGGTG GGGGTCACC      120
CACCOTTCAT ATCGGGGCTA CCGGCTTCCT CGGCTTGGGT GTTGTCGACA ACAACGGCAA      180
CGGCGCACGA GTCCAACGCG TGGTGGGGAG CCGTCCGGCG CCAAGTCTCG GCATCTCCAC      240
CGGCGACGTG ATCACCGCGG TCGACGGGCG TCCGATCAAC TCGGGCACCG CGATGGCGGA      300
CGCGCTTAAC GGGCATCATC CCGGTGACGT CATCTGGGTG AACTGGCAAA CCAAGTCGGG      360
CGGCACGCGT ACAGGGAACG TGACATTGGC CGAGGGACCC CCGGCTCAT TTGCTCGYGG      420
ATACGACCCG CCGGCGGGCC AATTGGA                                     447

```

(2) INFORMATION FOR SEQ ID NO:66:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1           5           10           15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20           25           30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35           40           45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50           55           60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65           70           75
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
80           85           90
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100          105          110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115          120          125
Gly Pro Pro Ala
130

```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

ATGAAGTTGA AGTTTGCTCG CTGAGTACT GCGATACTGG GTTGTGCAGC GCGCGTTGTG	50
TTTCTGCGCT CGGTTGCCAG CCGAGATCCA CTTGACCCGC ATCAGCCGGA CATGACGAAA	100
GGCTATTGCC CGGGTGGCCC ATGGGGTTTT GCGGACTTGG CCGTGTGCGA CCGCGAGAAG	150
TACCCGACAG GCTGGTTTTG GCACCACTGG ATGCAAAAGT GGTTTACCGG CCGACAGTTT	200
TACTTCGATT GTGTGACCG CGGTGAGCCC CTCCCGGCCC GCGCGCCACC GGTGTGTTGC	250
GGTGGGGCAA TTCCGTCGGA GCAGCCCAAC GCTCCCTGA	319

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Met	Lys	Leu	Lys	Phe	Ala	Arg	Leu	Ser	Thr	Ala	Ile	Leu	Gly	Cys	Ala	1	5	10	15
Ala	Ala	Leu	Val	Phe	Pro	Ala	Ser	Val	Ala	Ser	Ala	Asp	Pro	Pro	Asp	20	25	30	
Pro	His	Gln	Pro	Asp	Met	Thr	Lys	Gly	Tyr	Cys	Pro	Gly	Gly	Arg	Trp	35	40	45	
Gly	Phe	Gly	Asp	Leu	Ala	Val	Cys	Asp	Gly	Glu	Lys	Tyr	Pro	Asp	Gly	50	55	60	
Ser	Phe	Trp	His	Gln	Trp	Met	Gln	Thr	Trp	Phe	Thr	Gly	Pro	Gln	Phe	65	70	75	80
Tyr	Phe	Asp	Cys	Val	Ser	Gly	Gly	Glu	Pro	Leu	Pro	Gly	Pro	Pro	Pro	85	90	95	
Pro	Gly	Gly	Cys	Gly	Gly	Ala	Ile	Pro	Ser	Glu	Gln	Pro	Asn	Ala	Pro	100	105	110	

ESAT-6

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

{x1} SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGACAGAGC	AGCAGTGGAA	TTTCGCGGGT	ATCGAGGCGG	CGGCAAGCGC	AATCCAGGGA	60
AATGTACAGT	CCATTCATTC	CTTCCTTGAC	GAGGGGAAGC	AGTCCTGAC	CAAGCTCCCA	120
CGGCGCTGGG	CCCGTAGCGG	TTCCGAAAGG	TACC			154

(2) INFORMATION FOR SEQ ID NO:104:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met Thr Glu Ala Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1 5 10 15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
20 25 30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Trp Gly Gly Ser Gly Ser
35 40 45
Glu Ala Tyr
50

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/25005

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : A61K 39/095, 39/06, 39/06; C07K 1/00.
US CL : 424/240.1, 244.1, 185.1, 190.1, 192.1, 550/550.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/240.1, 244.1, 185.1, 190.1, 192.1, 550/550.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P	WO 99/51748 A2 (CORIXA CORPORATION) 14 October 1999, see entire document.	18-28 and 72-79
Y, P	HENDRICKSON et al. Mass spectrometric identification of Mtb81, a novel serological marker for tuberculosis. J. Clin. Microbiol. June 2000, Vol. 38, No. 6, pages 2354-2361, see entire document.	1-3, 18-28, 56-58 and 72-79
Y, P	BRANDT et al. ESAT-6 subunit vaccination against Mycobacterium tuberculosis. Infect. Immun. February 2000, Vol. 68, No. 2, pages 791-795, see entire document.	18-28 and 72-79

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	"P"	later documents published after the international filing date or priority date and not in conflict with the application but cited to understand the prototype or theory underlying the invention
"A" Document reflecting the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"B" earlier document published on or after the international filing date	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is considered with one or more other such documents, such combination being obvious to a person skilled in the art
"I" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"A"	document member of the same patent family
"U" Document reflecting to an oral disclosure, use, exhibition or other means		
"P" Document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

26 DECEMBER 2000

Date of mailing of the international search report

06 FEB 2001

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/26095

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y, P	ALDERSON et al. Expression cloning of an immunodominant family of Mycobacterium tuberculosis antigens using human CD4+ T cells. J. Exp. Med. 07 February 2000, Vol. 191, No. 3, pages 551-559, see entire document.	18-28 and 72-79
Y	COOLER et al. Molecular cloning and immunologic reactivity of a novel low molecular mass antigen of Mycobacterium tuberculosis. J. Immunol. 01 September 1998, Vol. 161, No. 5, pages 2356-2364, see entire document.	18-28 and 72-79
Y	ZIMMERMAN et al. Immunization with peptide heteroconjugates primes a T helper cell type 1-associated antibody (IgG2a) response that recognizes the native epitope on the 38-kDa protein of Mycobacterium tuberculosis. Vaccine Res. 1996, Vol. 5, No. 2, pages 103-118, see entire document.	18-28 and 72-79
Y	LEAO et al. Immunological and functional characterization of proteins of the Mycobacterium tuberculosis antigen 85 complex using synthetic peptides. J. Gen. Microbiol. 1993, Vol. 139, pages 1543-1549, see entire document.	18-28 and 72-79
Y	VORDERMEIER et al. Synthetic delivery system for tuberculosis vaccines: immunological evaluation of the M. tuberculosis 38 kDa protein entrapped in biodegradable PLG microparticles. Vaccine 1995, Vol. 13, No. 16, pages 1576-1582, see entire document.	18-28 and 72-79
Y	LOWRIE et al. Progress towards a new tuberculosis vaccine. BioDrugs September 1998, Vol. 10, No. 3, pages 201-213, see entire document.	18-28 and 72-79

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/48095**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(a)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos. 1-5, 18-28, 56-58 and 78-79.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/00995

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

DIALOG, MEDLINE, EMBASE, WEST, BIOSIS, PASCAL

Mycobact², Mos, MTB81, TbRa, sskD, Tb88-1, MTB11, FL TbH4, HTCC#1, Mtb40, TbH9, MTCC#2, MTB41, DPEP, DPPD, TbRas, TbRas1, Mtb40, MTB82, Erd4, Mtb16, FL TbRas, Mtb40, DPV, MTB4, MSI, MTB4, MTI, MTB4, MTI-A, ESAT-6, alpha-crystalline, 8S complex.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 1.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claims 1-3 and 50-58, draws to a pharmaceutical composition comprising a mycobacterial MTB81 antigen and an Mos antigen and a method of eliciting an immune response by administering the same.

Group II, claims 4-6, 59-61, 107 and 108, draws to a pharmaceutical composition comprising a mycobacterial TbRa, a 55 kD antigen, a Tb88-1 antigen and a FL TbH4 antigen, a fusion protein comprising the same and a method of eliciting an immune response by administering the composition.

Group III, claims 7-14, 62-68 and 109-115, draws to a pharmaceutical composition comprising a mycobacterial HTCC#1 and a TbH9 antigen, a fusion protein comprising the same and a method of eliciting an immune response by administering the composition.

Group IV, claims 15-17, 69-71, 116 and 118, draws to a pharmaceutical composition comprising a mycobacterial TbRa antigen and an HTCC#1 antigen, a fusion protein comprising the same and a method of eliciting an immune response by administering the composition.

Group V, claims 80-88 and 90-92, an expression cassette comprising nucleic acids encoding mycobacterial MTB81 and Mos antigens and a method of eliciting an immune response by administering the same.

Group VI, claims 89-95 and 93-97, draws to an expression cassette comprising nucleic acids encoding mycobacterial TbRa, a 55 kD antigen, a Tb88-1 antigen and a FL TbH4 antigen and a method of eliciting an immune response by administering the same.

Group VII, claims 97-99 and 94-96, draws to an expression cassette comprising nucleic acids encoding mycobacterial HTCC#1 and TbH9 antigens and a method of eliciting an immune response by administering the same.

Group VIII, claims 100-106 and 98-99, draws to an expression cassette comprising nucleic acids encoding mycobacterial TbRa and HTCC#1 antigens and a method of eliciting an immune response by administering the same.

Claims 13-45 and 72-79 are considered linking claims and would be joined with one of inventions I, II, III and IV, if elected.

Claims 51-55 and 100-106 are considered linking claims and would be joined with one of inventions V, VI, VII and VIII, if elected.

The inventions listed as Groups I through VIII do not relate to a single inventive concept under PCT Rule 1.1 because, under PCT Rule 1.1, they lack the same or corresponding special technical features for the following reasons:

Inventions I through IV are drawn to compositions comprising distinct mycobacterial antigens and methods of using the same. Inventions V through VIII are drawn to four different expression cassettes and methods of using the same. Clearly, the special technical features of inventions I through VIII is not a unifying feature and there is no single general inventive concept underlying the plurality of claimed inventions of the present application in the sense of PCT Rule 1.1. Consequently, the application lacks unity of invention.